Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 02:21:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524903.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10524903 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524903.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 02:21:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524903.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	725,830
Mapped reads	674,681 / 92.95%
Unmapped reads	51,149 / 7.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,665 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	22,771 / 3.14%
Duplication rate	2.71%
Clipped reads	676,862 / 93.25%

2.2. ACGT Content

Number/percentage of A's	10,250,920 / 25.79%
Number/percentage of C's	7,195,944 / 18.11%
Number/percentage of T's	12,375,602 / 31.14%
Number/percentage of G's	9,920,615 / 24.96%
Number/percentage of N's	282 / 0%
GC Percentage	43.07%

2.3. Coverage

Mean	0.0128

Standard Deviation	0.1484

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

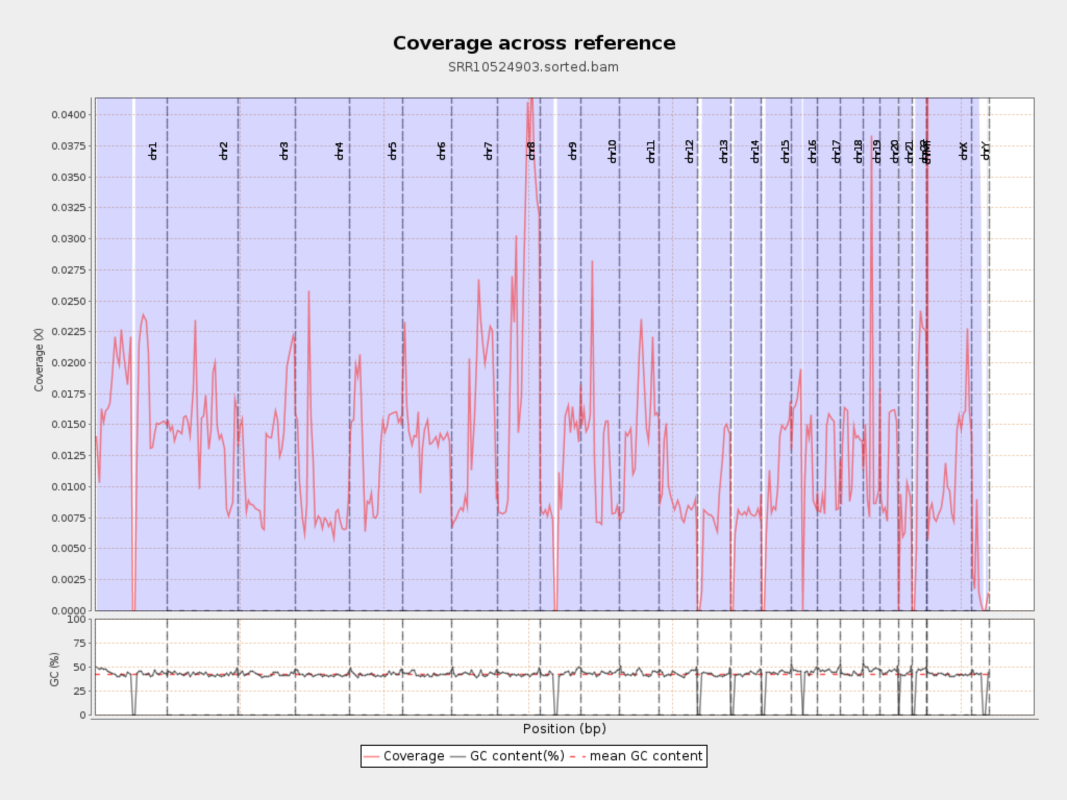
General error rate	0.5%
Mismatches	195,113
Insertions	2,409
Mapped reads with at least one insertion	0.36%
Deletions	7,628
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.15%

2.6. Chromosome stats

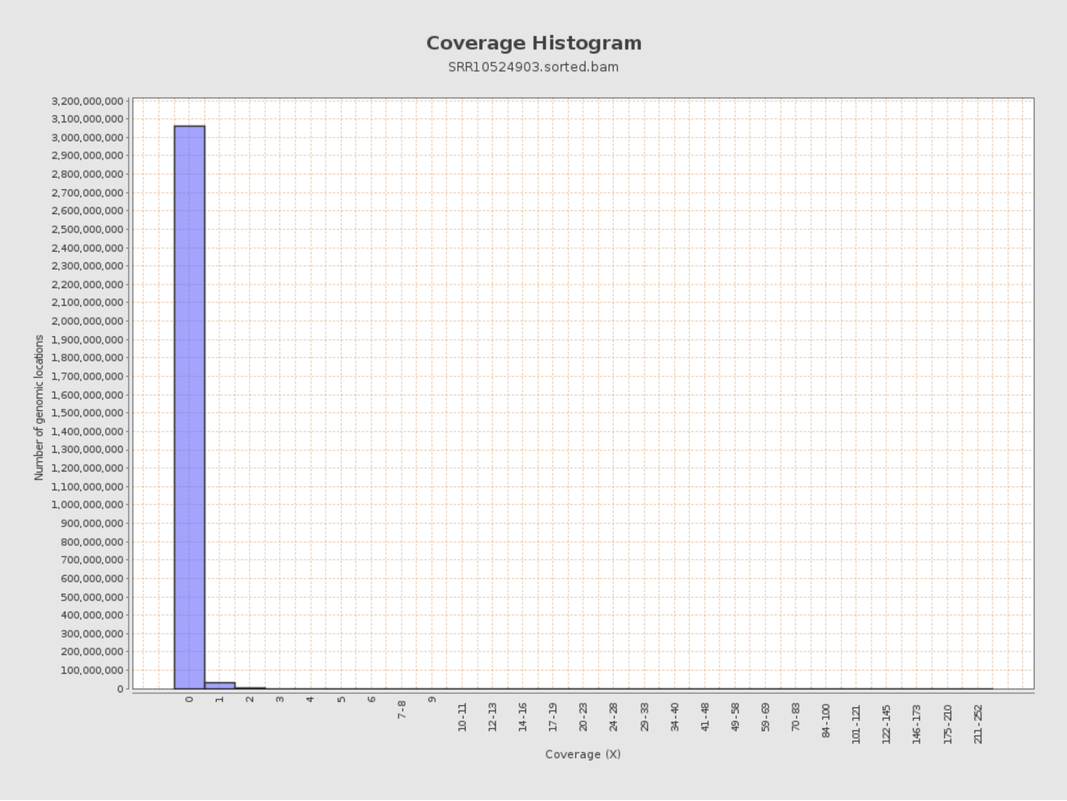
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4138812	0.0166	0.2368
chr2	243199373	3541193	0.0146	0.1729
chr3	198022430	2594174	0.0131	0.1218
chr4	191154276	1767451	0.0092	0.1229
chr5	180915260	2469634	0.0137	0.1243
chr6	171115067	2464906	0.0144	0.1309
chr7	159138663	2411157	0.0152	0.1732

chr8	146364022	3490684	0.0238	0.1992
chr9	141213431	1459471	0.0103	0.1219
chr10	135534747	1714950	0.0127	0.1659
chr11	135006516	2045504	0.0152	0.141
chr12	133851895	1230927	0.0092	0.1029
chr13	115169878	955933	0.0083	0.0973
chr14	107349540	727394	0.0068	0.0886
chr15	102531392	1024884	0.01	0.1067
chr16	90354753	1165963	0.0129	0.1242
chr17	81195210	907865	0.0112	0.1159
chr18	78077248	1034741	0.0133	0.1785
chr19	59128983	820579	0.0139	0.175
chr20	63025520	763197	0.0121	0.1194
chr21	48129895	357714	0.0074	0.1062
chr22	51304566	769351	0.015	0.1306
chrMT	16571	7827	0.4723	0.7188
chrX	155270560	1766240	0.0114	0.1171
chrY	59373566	125859	0.0021	0.0892

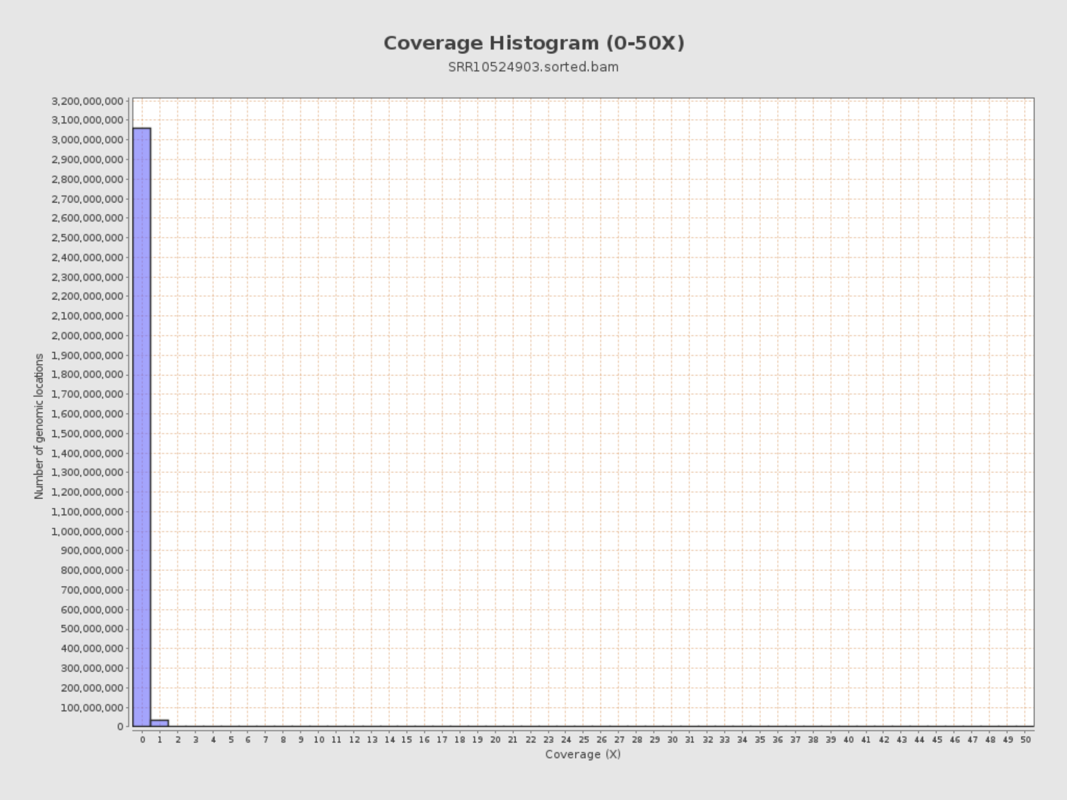
3. Results : Coverage across reference



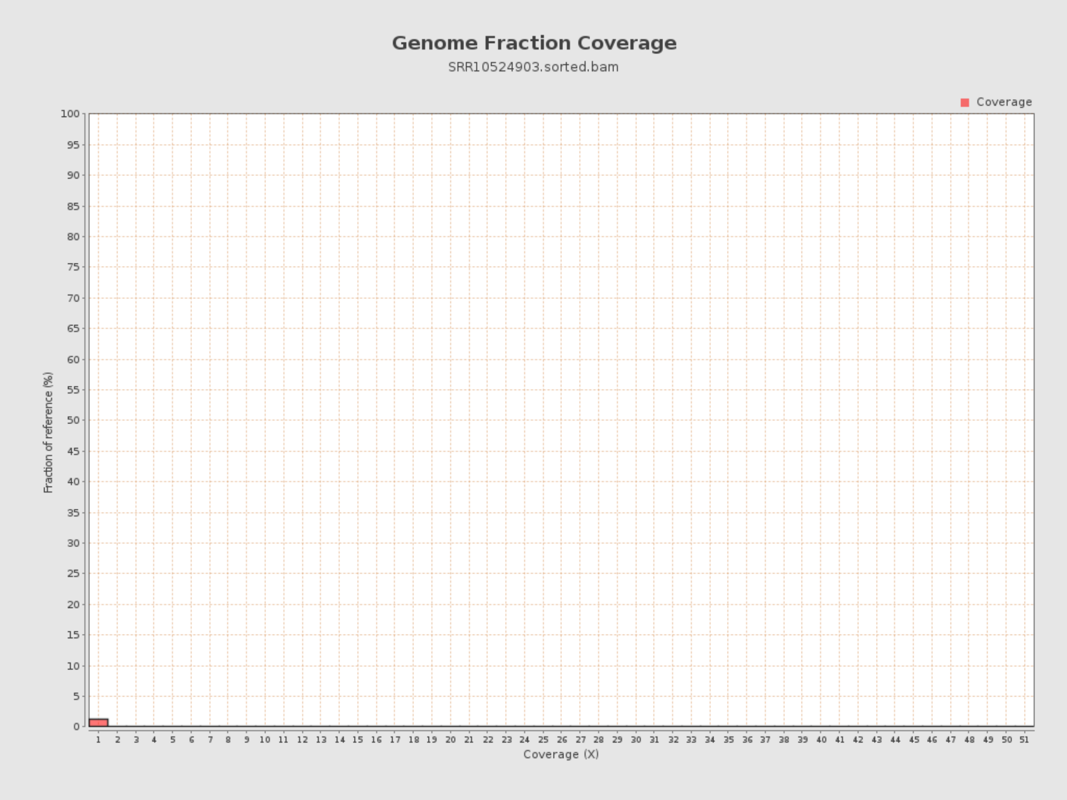
4. Results : Coverage Histogram



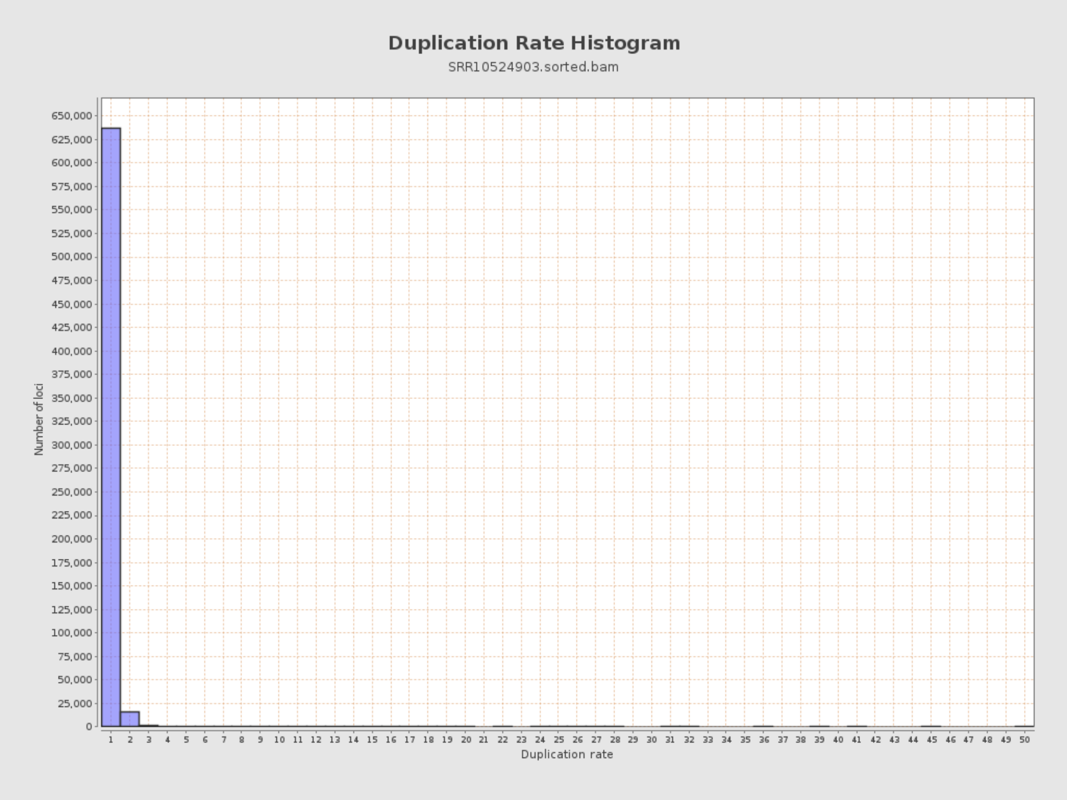
5. Results : Coverage Histogram (0-50X)



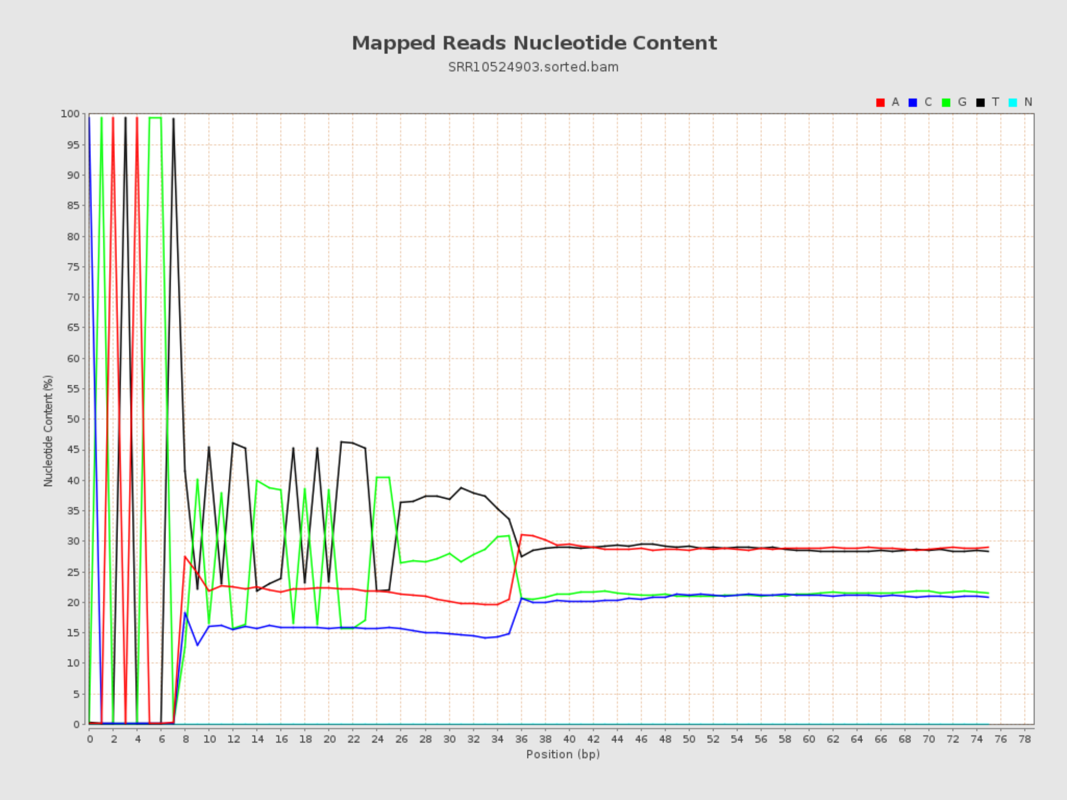
6. Results : Genome Fraction Coverage



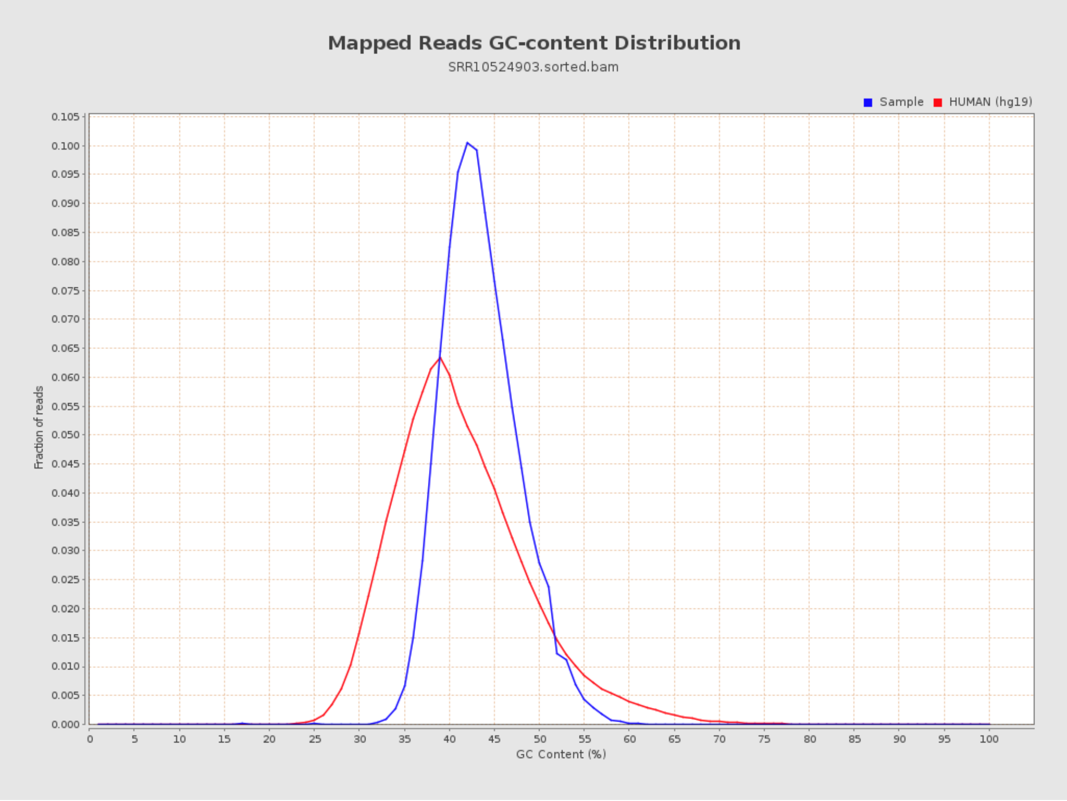
7. Results : Duplication Rate Histogram



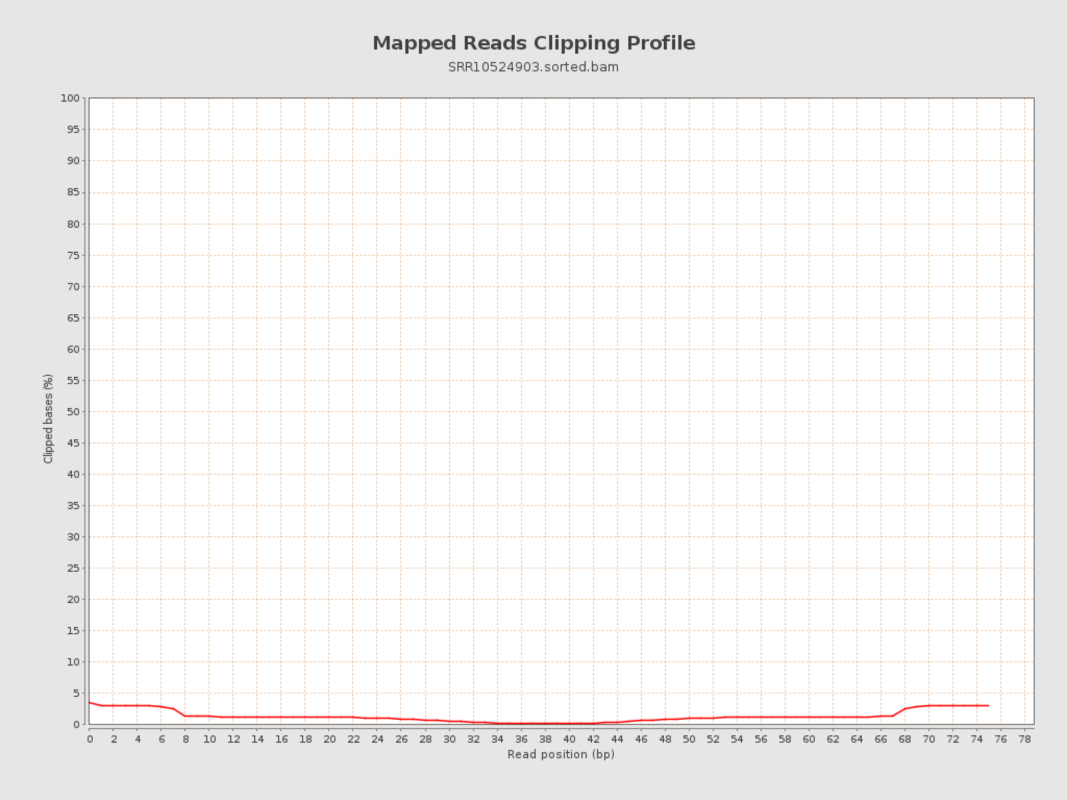
8. Results : Mapped Reads Nucleotide Content



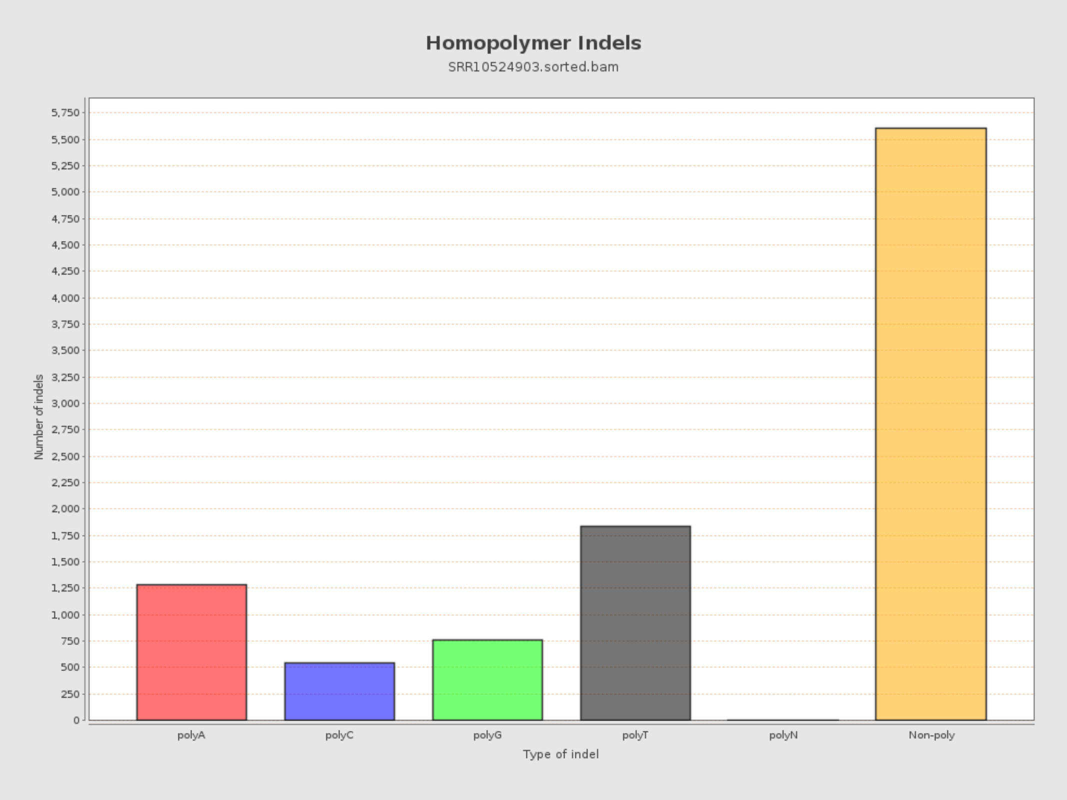
9. Results : Mapped Reads GC-content Distribution



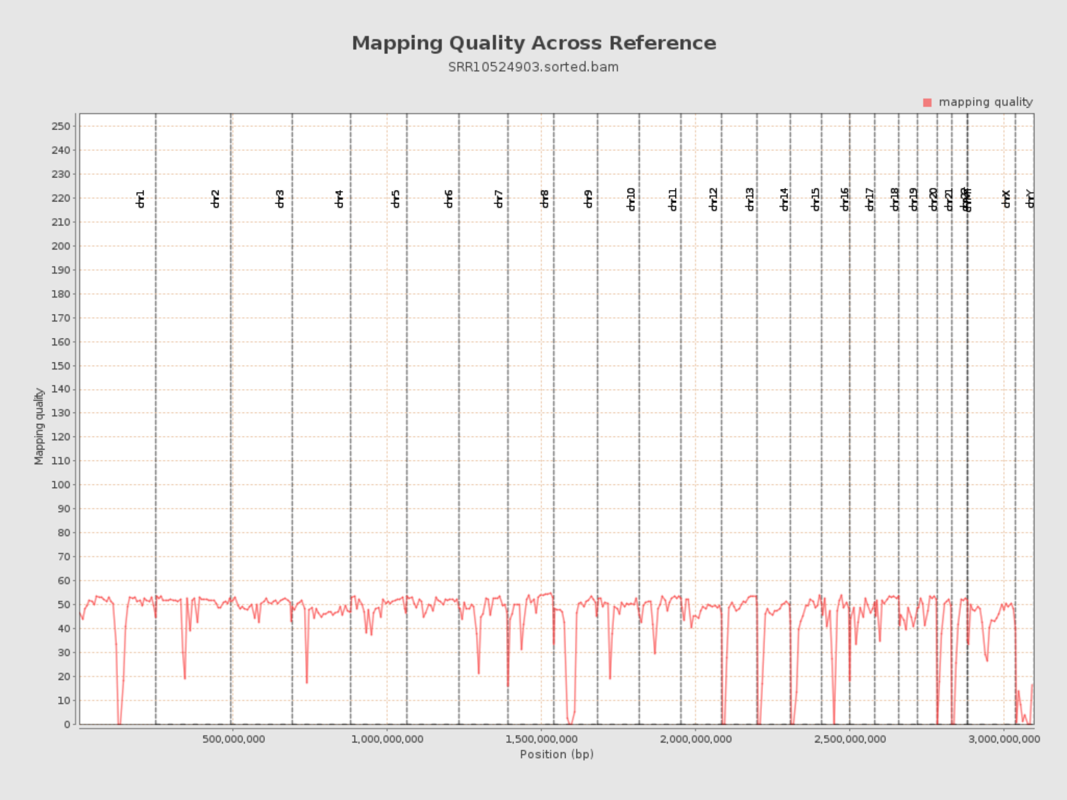
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram